

GCCGCGGCGCCCCGAGGCGGGAGCAAGAGGCGCCGGGAGCCGCGAGGATCCACC
 GCCGCGGCGCGCGCCATGGAGCCCCGAGTGAGCGCGCGGCGCTCCCCGGCCGCCG
 GACGACATGGAAACGGCGCCGACCCGGGCCCCCTCCGCGCCGCGCCGCGCGCT
 GCTGCTGCTGGTGCTGTACTGCAGCTTGGTCCCCGCGCGGCCTCACCGCTCC
 TGTTGTTTGCCAACCGCCGGGATGTGCGGCTAGTGGATGCCGGCGGAGTGAAG
 CTGGAGTCCACCATTTGTGGCCAGTGGCCTGGAGGATGCAGCTGCTGTAGACTT
 CCAGTTCTCCAAGGGTGCTGTGTACTGGACAGATGTGAGCGAGGAGGCCATCA
 AACAGACCTACCTGAACCAGACTGGAGCTGCTGCACAGAACATTGTCATCTCG
 GGCTTCGTGTCACCTGATGGCCTGGCCTGTGACTGGGTTGGCAAGAAGCTGTA
 CTGGACGGACTCCGAGACCAACCGCATTTGAGGTTGCCAACCTCAATGGGACGT
 CCCGTAAGGTTCTCTTCTGGCAGGACCTGGACCAGCCAAGGGCCATTGCCCTG
 GATCCTGCACATGGGTACATGTACTGGACTGACTGGGGGGAAGCACCCCGGAT
 CGAGCGGGCAGGGATGGATGGCAGTACCCGGAAGATCATTGTAGACTCCGACA
 TTTACTGGCCCAATGGGCTGACCATCGACCTGGAGGAACAGAAGCTGTACTGG
 GCCGATGCCAAGCTCAGCTTCATCCACCGTGCCAACCTGGACGGCTCCTTCCG
 GCAGAAGGTGGTGGAGGGCAGCCTCACTCACCTTTTGCCCTGACACTCTCTG
 GGGACACACTCTACTGGACAGACTGGCAGACCCGCTCCATCCACGCCTGCAAC
 AAGTGGACAGGGGAGCAGAGGAAGGAGATCCTTAGTGCTCTGTACTCACCCAT
 GGACATCCAAGTGCTGAGCCAGGAGCGGCAGCCTCCCTTCCACACACCATGCG
 AGGAGGACAACGGTGGCTGTTCCCACCTGTGCCTGCTGTCCCCGAGGGAGCCT
 TTCTACTCCTGTGCCTGCCCCACTGGTGTGCAGTTGCAGGACAATGGCAAGAC
 GTGCAAGACAGGGGCTGAGGAAGTGCTGCTGCTGGCTCGGAGGACAGACCTGA
 GGAGGATCTCTCTGGACACCCCTGACTTCACAGACATAGTGCTGCAGGTGGGC
 GACATCCGGCATGCCATTGCCATTGACTACGATCCCCTGGAGGGCTACGTGTA
 CTGGACCGATGATGAGGTGCGGGCTATCCGCAGGGCGTACCTAGATGGCTCAG
 GTGCGCAGACACTTGTGAACACTGAGATCAATGACCCCGATGGCATTTGCTGTG
 GACTGGGTGCCCCGGAACCTCTACTGGACAGATACAGGCACTGACAGAATTGA
 GGTGACTCGCCTCAACGGCACCTCCCGAAAGATCCTGGTATCTGAGGACCTGG
 ACGAACC GCGAGCCATTGTGTTGCACCCTGTGATGGGCCTCATGTACTGGACA
 GACTGGGGGGAGAACCCCAAATCGAATGCGCCAACCTAGATGGGAGAGATCG
 GCATGTCCTGGTGAACACCTCCCTTGGGTGGCCCAATGGACTGGCCCTGGACC
 TGCAGGAGGGCAAGCTGTACTGGGGGGATGCCAAAACCTGATAAAATCGAGGTG
 ATCAACATAGACGGGACAAAGCGGAAGACCCTGCTTGAGGACAAGCTCCCACA
 CATTTTTGGGTTTCACTGCTGGGGGACTTCATCTACTGGACCGACTGGCAGA
 GACGCAGTATTGAAAGGGTCCACAAGGTCAAGGCCAGCCGGGATGTCATCATT
 GATCAACTCCCCGACCTGATGGGACTCAAAGCCGTGAATGTGGCCAAGGTTGT
 CGGAACCAACCCATGTGCGGATGGAAATGGAGGGTGCAGCCATCTGTGCTTCT
 TCACCCACGTCGCCACCAAGTGTGGCTGCCCCATTGGCCTGGAGCTGTTGAGT
 GACATGAAGACCTGCATAATCCCCGAGGCCTTCTGGTATTCACCAGCAGAGC
 CACCATCCACAGGATCTCCCTGGAGACTAACAACAACGATGTGGCTATCCCAC
 TCACGGGTGTCAAAGAGGCCTCTGCACTGGACTTTGATGTGTCCAACAATCAC

FIGURE 1A

ATCTACTGGACTGATGTTAGCCTCAAGACGATCAGCCGAGCCTTCATGAATGG
 GAGCTCAGTGGAGCACGTGATTGAGTTTGGCCTCGACTACCCTGAAGGAATGG
 CTGTGGACTGGATGGGCAAGAACCTCTATTGGGCGGACACAGGGACCAACAGG
 ATTGAGGTGGCCCCGGCTGGATGGGCAGTTCCGGCAGGTGCTTGTGTGGAGAGA
 CCTTGACAACCCAGGTCTCTGGCTCTGGATCCTACTAAAGGCTACATCTACT
 GGACTGAGTGGGGTGGCAAGCCAAGGATTGTGCGGGCCTTCATGGATGGGACC
 AATTGTATGACACTGGTAGACAAGGTGGGCGGGCCAACGACCTCACCATTGA
 TTATGCCGACCAGCGACTGTACTGGACTGACCTGGACACCAACATGATTGAGT
 CTTCCAACATGCTGGGTGAGGAGCGCATGGTGATAGCTGACGATCTGCCCTAC
 CCGTTTGGCCTGACTCAATATAGCGATTACATCTACTGGACTGACTGGAACCT
 GCATAGCATTGAACGGGCGGACAAGACCAGTGGGCGGAACCGCACCCCTCATCC
 AGGGTCACCTGGACTTCGTTCATGGACATCCTGGTGTTCCTCCTCCCGTCAG
 GATGGCCTCAACGACTGCGTGCACAGCAATGGCCAGTGTGGGCAGCTGTGCCT
 CGCCATCCCCGGAGGCCACCGCTGTGGCTGTGCTTCACACTACACGCTGGACC
 CCAGCAGCCGCAACTGCAGCCCCGCCCTCCACCTTCTTGCTGTTTCAGCCAGAAA
 TTTGCCATCAGCCGGATGATCCCCGATGACCAGCTCAGCCCGGACCTTGTCTCT
 ACCCCTTCATGGGCTGAGGAACGTCAAAGCCATCAACTATGACCCGCTGGACA
 AGTTCATCTACTGGGTGGACGGGCGCCAGAACATCAAGAGGGCCAAGGACGAC
 GGTACCCAGCCCTCCATGCTGACCTCTCCAGCCAAAGCCTGAGCCCAGACAG
 ACAGCCACACGACCTCAGCATTGACATCTACAGCCGGACACTGTTCTGGACCT
 GTGAGGCCACCAACACTATCAATGTCCACCGGCTGGATGGGGATGCCATGGGA
 GTGGTGCTTCGAGGGGACCGTGACAAGCCAAGGGCCATTGCTGTCAATGCTGA
 GCGAGGGTACATGTACTTTACCAACATGCAGGACCATGCTGCCAAGATCGAGC
 GAGCCTCCCTGGATGGCACAGAGCGGGAGGTCTCTTACCACAGGCCTCATC
 CGTCCCGTGGCCCTTGTGGTGGACAATGCTCTGGGCAAGCTCTTCTGGGTGGA
 TGCCGACCTAAAGCGAATCGAAAGCTGTGACCTCTCTGGGGCCAACCGCCTGA
 CCCTGGAAGATGCCAACATCGTACAGCCAGTAGGTCTGACAGTGCTGGGCAGG
 CACCTCTACTGGATCGACCGCCAGCAGCAGATGATCGAGCGCGTGGAGAAGAC
 CACTGGGGACAAGCGGACTAGGGTTTCAGGGCCGTGTCACCCACCTGACAGGCA
 TCCATGCCGTGGAGGAAGTCAGCCTGGAGGAGTTCTCAGCCCATCCTTGTGCC
 CGAGACAATGGCGGCTGCTCCACATCTGTATCGCCAAGGGTGATGGAACACC
 GCGCTGCTCGTGCCCTGTCCACCTGGTGCTCCTGCAGAACCTGCTGACTTGTG
 GTGAGCCTCCTACCTGCTCCCCTGATCAGTTTGCATGTACCACTGGTGAGATC
 GACTGCATCCCCGGAGCCTGGCGCTGTGACGGCTTCCCTGAGTGTGCTGACCA
 GAGTGATGAAGAAGGCTGCCCAGTGTGCTCCGCCTCTCAGTTCCCCTGCGCTC
 GAGGCCAGTGTGTGGACCTGCGGTTACGCTGCGACGGTGAGGCCGACTGCCAG
 GATCGCTCTGATGAAGCTAACTGCGATGCTGTCTGTCTGCCCAATCAGTTCCG
 GTGCACCAGCGGCCAGTGTGTCCTCATCAAGCAACAGTGTGACTCCTTCCCCG
 ACTGTGCTGATGGGTCTGATGAGCTCATGTGTGAAATCAACAAGCCACCCTCT
 GATGACATCCCAGCCCACAGCAGTGCCATTGGGCCCCGTCATTGGTATCATCCT
 CTCCCTCTTCGTTCATGGGCGGGGTCTACTTTGTCTGCCAGCGTGTGATGTGCC

FIGURE 1B

[illegible]

1

[illegible]

419

METAPTRAPPPPPPLLLLVLVYCSLVPAAASPLLLFANRRDVRLVDAGGVKLE
 STIVASGLEDAAAVDFQFSKGAVYWTDVSEEAIKQTYLNQTGAAAQNIVISGL
 VSPDGLACDWVGKKLYWTDSETNRIEVANLNGTSRKVLFWQDLDPRAIALDP
 AHGYMYWTDWGEAPRIERAGMDGSTRKIIIVDSDIYWPNGLTIDLEEOKLYWAD
 AKLSFIHRANLDGSFRQKVVEGSLTHPFALTLSGDTLYWTDWQTRSIHACNKW
 TGEQRKEILSALYSPMDIQVLSQERQPPFHTPCEEDNGGCShLCLLSPREPFY
 SCACPTGVQLQDNGKTCKTGAEVLLLARRTDLRRI SLDTPDFTDIVLQVGDI
 RHAIAIDYDPLEGYVYWTDDEVRAIRRAYLDGSGAQTLVNTEINDPDGIAVDW
 VARNLYWTDGTGTDRIEVTRLNGTSRKILVSEDLDEPRAIVLHPVMGLMYWTDW
 GENPKIECANLDGRDRHVLVNTSLGWPNGLALDLQEGKLYWGDADTKIEVIN
 IDGTRKKTLLLEDKLP HIFGFTLLGDFIYWTDWQRRS IERVHKVKASRDVIIDQ
 LPDLMGLKAVNVAKVVG TNPCADGNGGCShLCFFT PRATKCGCPIGLELLSDM
 KTCIIPEAF LVFTSRATIHRI SLETNNNDVAIPLTGVKEASALDFDVSNNH IY
 WTDVSLKTI SRAFMNGSSVEHVIEFGLDYPEGMAVDWMGKNLYWADTGTNRIE
 VARLDGQFRQVLVWRDL DNPRSLALDPTKGYIYWTEWGGKPRIVRAFMDGTNC
 MTLVDKVGRANDLTIDYADQRLYWTDLDTNMIESSNMLGQERMVIADDL PYPF
 GLTQYSDYIYWTDWNLHSIERADKTSGRNRTLIQGHLD FVMDILVFHSSRQDG
 LNDCVHSNGQCGQLCLAI PGGHRCGCASHYTLDPSSRNCSPPSTFLLFSQKFA
 ISRMIPDDQLSPDLVLPLHGLRNVKAINYDPLDKFIYWVDGRQNIKRAKDDGT
 QPSMLTSPS QSLSPDRQPHDLSIDIYSRTLFWTCEATNTINVHRLDGDAMGVV
 LRGDRDKPRAIAVNAERGYMYFTNMQDHA AKIERASLDGTEREVLF TTGLIRP
 VALVVDNALGKLFWVDADLKRIESCDLSGANRLTLEDANIVQPVGLTVLGRHL
 YWIDRQQQM IERVEKTTGDKRTRVQGRVTHLTGIHAVEEV SLEEFSAHPCARD
 NGGCShICIAKGDGT PRCSCP VHLVLLQNL LTCGEPPTCSPDQFACTTGEIDC
 IPGAWRCDGFPECADQSDEEGCPVCSASQFPCARGQCVDLRLRCDGEADCQDR
 SDEANCD AVCLPNQFRCTSGQCVLIKQQCDSFPDCADGSDELMCEINKPPSDD
 IPAHSSAIGPVIGIILSLFVMGGVYFVCQRVMCQRYTGASGPF PHEYVGGAPH
 VPLNFIAPGGSQHGPFGIPCSKSVMSMSLVGGRGSVPLYDRNHVTGASSSS
 SSSTKATLYPPILNPPPSPATDPSLYNVDVFYSSGIPATARPYR PYVIRGMAP
 PTTPCSTDVCDSDYSISRWKSSKYLDLNSDSDPYPPPTPHSQYLSAEDSCP
 PSPGTERS YCHLFP PPPSPCTDSS (SEQ ID NO: 8)

2

FIGURE 2

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Construct

Gene: 193 GI Number(s): 6678715
 Gene Family: EGF domain protein
 Gene Subfamily: Low-density lipoprotein receptor
 Gene Sequence: full-length cDNA, Mouse

underlined = deleted in targeting construct

[] = sequence flanking Neo insert in targeting construct

GCGCGCGCGCGCGAGGCGGGAGCAAGAGGCGCGGGAGCGCGAGGATCCACCGCGCGCG
 CGCGCGCCATGGAGCCCGAGTGAAGCGCGCGCGCTCCCGCGCGCGGACGACATGGAAAC
 GGCGCGGACCGCGCGCGCGCTCCCGCGCGCGCGCGCGCTGCTGCTGCTGGTGTGTACTG
 CAGCTTGGTCCCGCGCGCGCGCTCACCCTCCTGTTGTTTGGCAACCGCGCGGATGTGCG
 GCTAGTGGATGCCGCGGAGTGAAGCTGGAGTCCACCATTGTGGCCAGTGGCCTGGAGGA
 TGCAGCTGCTGTAGACTTCCAGTTCTCCAAGGCTGCTGTGTACTGGACAGATGTGAGCGA
 GGAGGCCATCAAACAGACCTACCTGAACCAGACTGGAGCTGCTGCACAGAACATTGTCTAT
 CTCGGGCGCTCGTGTACCTGATGGCCTGGCCTGTGACTGGGTGGCAAGAAGCTGTACTG
 GACGGACTCCGAGACCAACCGCATTTGAGGTTGCCAACCTCAATGGGACGTCCCGTAAGGT
 TCTCTTCTGGCAGGACCTGGACCAGCCAAGGGCCATTGCCCTGGATCCTGCACATGGGTA
 CATGTACTGGACTGACTGGGGGGAAGCACCCCGGATCGAGCGGGCAGGGATGGATGGCAG
 TACCCGGAAGATCATTGTAGACTCCGACATTTACTGGCCCAATGGGCTGACCATCGACCT
 GGAGGAACAGAAGCTGTACTGGGCGGATGCCAAGCTCAGCTTCATCCACCGTGCCAACT
 GGACGGCTCCTTCCGGCAGAAGGTGGTGGAGGGCAGCCTCACTCACCTTTTGGCCTGAC
 ACTCTCTGGGGACACACTCTACTGGACAGACTGGCAGACCCGCTCCATCCACGCGCTGCAA
 CAAGTGGACAGGGGAGCAGAGGAAGGAGATCCTTAGTGCTCTGTACTACCCATGGACAT
 CCAAGTGCTGAGCCAGGAGCGGCAGCCTCCCTTCCACACACCATGCGAGGAGGACAACGG
 TGGCTGTTCCACCTGTGCTGCTGTCCCGAGGGAGCCTTTCTACTCCTGTGCTGCTGCCC
 CACTGGTGTGCACTTGCAGGACAATGGCAAGACGTGCAAGACAGGGGCTGAGGAAGTGCT
 GCTGCTGGCTCGGAGGACAGACCTGAGGAGGATCTCTCTGGACACCCCTGACTTCACAGA
 CATAGTGCTGCAGGTGGGCGACATCCGGCATGCCATTGCCATTGACTACGATCCCTTGGGA
 GGCTACGTGTACTGGACCGATGATGAGGTGCGGGCTATCCGCAGGGCGTACCTAGATGG
 CTCAGGTGCGCAGACACTTGTGAACACTGAGATCAATGACCCGATGGCATTGTGTGGA
 CTGGGTGCGCCGGAACCTCTACTGGACAGATACAGGCACTGACAGAATTGAGGTGACTCG
 CCTCAACGGCACCTCCCGAAAGATCCTGGTATCTGAGGACCTGGACGAACCGCGAGCCAT
 TGTGTTGCACCTGTGATGGGCCTCATGTACTGGACAGACTGGGGGGAGAACCCCAAAT
 CGAATGCGCCAACCTAGATGGGAGAGATCGGCATGTCCTGGTGAACACCTCCCTTGGGTG
 GCGCAATGGACTGGCCTGGACCTGCAGGAGGGCAAGCTGTACTGGGGGGATGCCAAAAC
 TGATAAAATCGAGGTGATCAACATAGACGGGACAAAGCGGAAGACCTGCTTGAGGACAA
 GCTCCACACATTTTGGGTTACACTGCTGGGGGACTTCATCTACTGGACCGACTGCCA
 GAGACGAGTATTGAAAGGGTCCACAAGGTCAAGGCCAGCCGGGATGTCATCATTGATCA
 ACTCCCGACCTGATGGGACTCAAAGCCGTGAATGTGCCAAGGTTGTGCGGAACCAACCC
 ATGTGCGGATGGAAATGGAGGGTGCAGCCATCTGTGCTTCTTACCCACAGTGCCACCAA
 GTGTGGCTGCCCCATTGGCCTGGAGCTGTTGAGTGACATGAAGACCTGCATAATCCCCGA
 GGCTTCTCTGGTATTCACAGCAGAGCCACCATCCACAGGATCTCCCTGGAGACTAACAA
 CAACGATGTGGCTATCCCACTACGGGTGTCAAAGAGGCTCTGCCTGGACTTTGATGT
 GTCCACAATCACATCTACTGGACTGATGTTAGCCTCAAGACGATCAGCCGAGCCTTCAT
 GAATGGGAGCTCAGTGGAGCACGTGATTGAGTTTGGCCTCGACTACCTGAAGGAATGGC
 TGTGGACTGGATGGGCAAGAACCTCTATTGGGCGGACACAGGGACCAACAGGATTGAGGT
 GGCCCGGCTGGATGGGCAAGTTCGGGCGAGGTGCTTGTGTGGAGAGACCTTGACAACCCAG
 GTCTCTGGCTCTGGATCCTACTAAAGGCTACATCTACTGGACTGAGTGGGGTGGCAAGCC
 AAGGATTGTGCGGGCCTTCATGGATGGGACCAATTGTATGACACTGGTAGACAAGGTGGG
 CCGGGCCAACGACCTCACCATTGATTATGCCGACGAGGACTGTACTGGACTGACCTGGA
 CACCAACATGATTGAGTCTTCCAACATGCTGGGTGAGGAGGCGATGCTGATAGCTGACGA

FIGURE 3A

TCTGCCCTACCCGTTTGGCCTGACTCAATATAGCGATTACATCTACTGGACTGACTGGAA
 CCTGCATAGCATTGAACGGGGCGGACAAGACCAGTGGGCGGAACCGCACCCCTCATCCAGGG
 TCACCTGGACTTCGTCATGGACATCCTGGTGTTCACCTCCTCCCGTCAGGATGGCCTCAA
 CGACTGCGTGCACAGCAATGGCCAGTGTGGGCAGCTGTGCCTCGCCATCCCCGGAGGCCA
 CCGCTGTGGCTGTGCTTCACACTACACGCTGGACCCAGCAGCCGCAACTGCAGCCCCGCC
 CTCCACCTTCTTGTGTTCAGCCAGAAATTGCCATCAGCCGGATGATCCCCGATGACCA
 GCTCAGCCCCGACCTTGTCTACCCCTTCATGGGGTGAGGAACGTCAAAGCCATCAACTA
 TGACCCGCTGGACAAGTTCATCTACTGGGTGGACGGGCGCCAGAACATCAAGAGGGCCAA
 GGACGACGGTACCCAGCCCTCCATGCTGACCTCTCCAGCCAAAGCCTGAGCCCAGACAG
 ACAGCCACACGACCTCAGCATTGACATCTACAGCCGGACACTGTTCTGGACCTGTGAGGC
 CACCAACACTATCAATGTCCACCGGCTGGATGGGGATGCCATGGGAGTGGTGTCTTCGAGG
 GGACCGTGACAAGCCAAGGGCCATTGCTGTCAATGCTGAGCGAGGGTACATGTACTTTAC
 CAACATGCAGGACCATGCTGCCAAGATCGAGCGAGCCTCCCTGGATGGCACAGAGCGGGA
 GGTCTCTTACCACAGGCCTCATCCGTCCCGTGGCCCTTGTGGTGGACAATGCTCTGGG
 CAAGCTCTTCTGGGTGGATGCCGACCTAAAGCGAATCGAAAGCTGTGACCTCTCTG [GGG
 CCAACCGCTGACCCTGGAAGATGCCAACATCGTACAGCCAGTAGGTCTGACAGTGTCTGG
 GCAGGCACCTCTACTGGATCGACCGCCAGCAGATGATCGAGCGCGTGGAGAAGACC]
ACTGGGGACAAGCGGACTAGGGTTTCAGGGCCCGTGTCACCCCACC [TGACAGGCATCCATGC
 CGTGGAGGAAGTCAGCCTGGAGGAGTTCT] CAGCCCATCCTTGTGCCCGAGACAATGGCG
 GCTGCTCCCATCTGTATCGCCAAGGGTGATGGAACACCGCGCTGCTCGTGGCCTGTCC
 ACCTGGTGTCTCTGCAGAACCTGTGACTTGTGGTGAGCCTCCTACCTGCTCCCTGTATC
 AGTTTGCATGTACCACTGGTGAGATCGACTGCATCCCCGGAGCCTGGCGCTGTGACGGCT
 TCCCTGAGTGTGCTGACCAGAGTGTGAAGAAGGCTGCCAGTGTGCTCCGCCCTCTCAGT
 TCCCCGTGCGCTCGAGGCCAGTGTGTGGACCTGCGGTTACGCTGCGACGGTGAGGCCGACT
 GCCAGGATCGCTCTGATGAAGCTAACTGCGATGCTGTCTGTCTGCCCAATCAGTTCCGGT
 GCACCAGCGGCCAGTGTGTCTCATCAAGCAACAGTGTGACTCCTTCCCCGACTGTGTCTG
 ATGGGTCTGATGAGCTCATGTGTGAAATCAACAAGCCACCCCTCTGATGACATCCAGCCC
 ACAGCAGTGCCATTGGGCCCCGTCAATTGGTATCATCCTCTCCCTCTTCGTCATGGGCGGGG
 TCTACTTTGTCTGCCAGCGTGTGATGTGCCAGCGCTACACAGGGGCCAGTGGGCCCTTTC
 CCCACGAGTATGTTGGTGGAGCCCTCATGTGCCTCTCAACTTCATAGCCCCAGGTGGCT
 CACAGCACGGTCCCTTCCCAGGCATCCCGTGCAGCAAGTCCGTGATGAGCTCCATGAGCC
 TGGTGGGGGGGGCGCGGCAGCGTGCCCCCTCTATGACCGGAATCACGTCACTGGGGCCCTCAT
 CCAGCAGCTCGTCCAGCACAAAGGCCACACTATATCCGCCGATCCTGAACCCACCCCGT
 CCCCCGCCACAGACCCCTCTCTTACAACGTGGACGTGTTTTATTCTTCAGGCATCCCCGG
 CCACCGCTAGACCATAACAGGCCCTACGTCATTGAGGTATGGCACCCCCAACACACCGT
 GCAGCACAGATGTGTGTGACAGTGAATGACTACAGCATCAGTCTGGAAGAGCAGCAAATACT
 ACCTGGACTTGAATTCGGACTCAGACCCCTACCCCCCCCCCGCCCCCCCCACAGCCAGT
 ACCTATCTGCAGAGGACAGCTGCCACCCCTCACCAGGCACTGAGAGGAGTTACTGCCACC
 TCTTCCCCGGCCCCACCGTCCCCCTGCACGGACTCGTCTGACCTCGGCCGTCCACCCGGC
 CCTGCTGCCTCCCTGTAAATATTTTAAATATGAACAAAGGAAAAATATATTTTATGATT
 TAAAAAATAAATATAATTGGGGTTTTTAACAAGTGAGAAATGTGAGCGGTGAAGGGGTGG
 GCAGGGCTGGGAACTTTTCTAG

Gene Sequence
Structure *

3659 bp

Sequence Deleted

3701 bp

Size of full-length
cDNA: 5119 bp

FIGURE 3B

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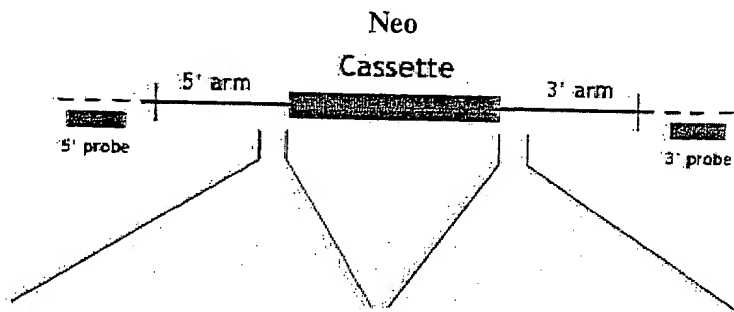
Targeting Vector* (genomic sequence)

Construct Number: 992

Arm Length:

5': 1.5 kb

3': 2.9 kb



———— Targeting Vector
 - - - - - Endogenous Locus

* Not drawn to scale

<p>5' >AAATATGCATTATCCTGAGCA CAGTGGGTCTGGCCCTTCACTTGG CTGCCACTCATGGAGCCTTTATGC TAACCACAGGGGCCAACCGCCTGA CCCTGGAAGATGCCAACATCGTAC AGCCAGTAGGTCTGACAGTGCTGG GCAGGCACCTCTACTGGATCGACC GCCAGCAGCAGATGATCGAGCGTG TGGAGAAGACC<3' (SEQ ID NO: 3) 3</p>	<p>5' >TCACTGGCATCCATGCAGTG: AGGAAGTCAGCCTGGAGGAGTTCT GTACGTGAGAGGGGACAGTGTTTG TGGTGGGGTCTCCTGGGGGAAGGT GAATCAGCCCTACTGGCATCAGAT GGGCTGCTGGTGCAAGAGCAGTGT GCCTGAGGAGCTCATGGGCTCAGC ACCGAAGGCCAGTGCATGTCCAGA TGTCTGCCTCT<3' (SEQ ID NO: 4) 4</p>
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FIGURE 3C

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Figure 1 consists of two histograms side-by-side. The left histogram is titled '2,1,-/-,Male' and the right is titled '2,1,+/-,Male'. Both histograms have 'n' on the x-axis (ranging from 0 to 15) and 'count' on the y-axis (ranging from 0 to 10). The distributions are roughly bell-shaped, peaking at n=10.

n	2,1,-/-,Male Count	2,1,+/-,Male Count
0	0	0
1	0	0
2	0	0
3	0	0
4	0	0
5	0	0
6	0	0
7	0	0
8	0	0
9	1	1
10	10	10
11	8	8
12	4	4
13	1	1
14	0	0
15	0	0



101250 04548860

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Phenotypic Data Summary - Open Field

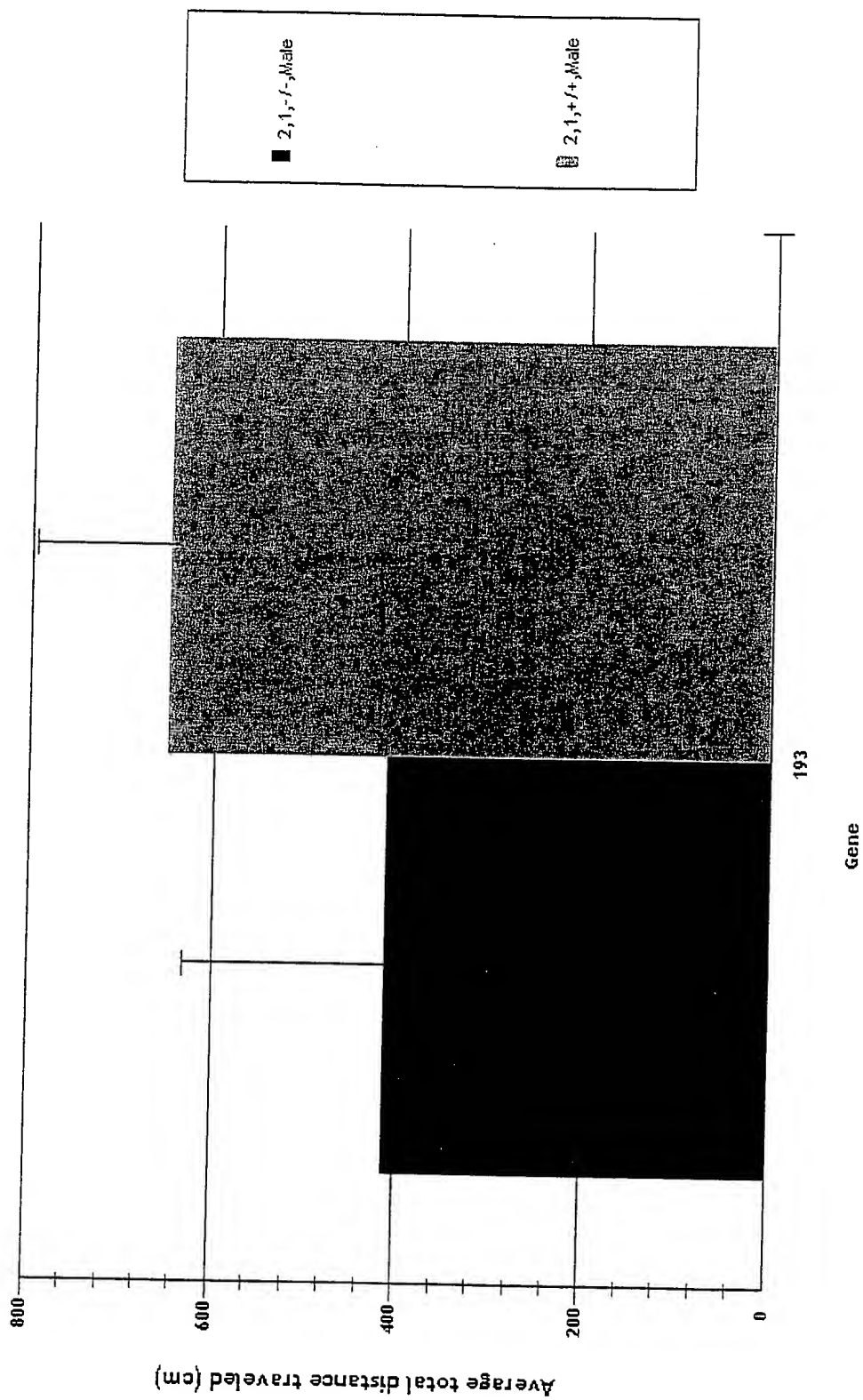


FIGURE 5